IN THE UNITED STATES DISTRICT COURT

FOR THE DISTRICT OF WYOMING

UNITED STATES OF AMERICA, Plaintiff, vs. ARAPAHO JAMES OLDMAN, MATTHEW WHITEPLUME, MONTY TABAHO, and JORI LAMEBULL, Defendants.	Case No. 18-CR-0020-SWS

ORDER DENYING DEFENDANT ARAPAHO OLDMAN'S MOTION TO EXCLUDE EXPERT TESTIMONY

This matter comes before the Court on Defendant Arapaho Oldman's *Motion to Exclude Expert Testimony on STRMix Generated DNA Inclusion or Match Statistic Under Daubert and Federal Rules of Evidence 702* (ECF No. 184). The Court having conducted an evidentiary hearing, considered the motion and briefs, oral argument, and being otherwise fully advised, finds as follows:

BACKGROUND

Defendant Oldman was charged with one count of first degree murder and aiding and abetting for the killing of Charles Dodge III (ECF No. 108). He has three co-defendants in the matter; Matthew Whiteplume who has also been charged with first degree murder and aiding and abetting, and Monty Tabaho and Jori Lamebull who have been charged with being accessories after the fact to first degree murder (*id.*). Relevant to this matter, it is alleged that Defendants Oldman and Whiteplume got into an altercation with

Mr. Dodge in a basement over alcohol, beat Dodge until he was unresponsive, and placed him in a crawlspace, where he died (ECF No. 184 at 6-7). Defendants Tabaho and Lamebull allegedly helped hide Mr. Dodge's body (*id.*). One form of evidence in this case is deoxyribonucleic acid (DNA) evidence (*id.* at 5). Twenty-three pieces of evidence were tested for DNA, two of those potentially inculpated Defendant Oldman (*id.*). These two pieces of evidence include multi-contributor swabs from the basement stairs and Defendant Oldman's shirt (*id.*). A probalistic genotyping software, STRMix™, was used to analyze the probabilities that Defendant Oldman and others could be included as contributors to the DNA mixtures. With a superseding indictment and various witnesses and evidence, the details of these allegations have changed and developed—but the Court need go no further for purposes of the instant motion. On December 3, 2018, Defendant Oldman filed this motion to exclude expert testimony on STRmix™ generated DNA inclusion or match statistics for evidence Items 12 and 53 (*see generally id.*). The government filed its tardy response on December 17, 2018 (ECF No. 205). Defendant filed an unauthorized Reply to the Response on December 19, 2018 (ECF No. 207) and the Court conducted and evidentiary hearing and heard oral arguments from counsel on December 21, 2018.

At issue in Defendant's Motion to Exclude is the admissibility of STRmix™ DNA test results from four contributors on two items of evidence, Exhibit No. 12 (swab from base of basement steps where alleged murder occurred) and Exhibit No. 53 (a stain on the outside front of Defendant Oldman's shirt). Defendant asserts the FBI Lab's DNA results obtained for these two items exceeded the limits of its internal validation for STRmix, version 2.4 (ECF No. 207 at 1-2). The Government asserts that the STRmix™ DNA test results on these items of evidence was derived from scientifically reliable methods and any

alleged deficiencies or lack of certainty goes to the weight not the admissibility of this DNA evidence (ECF No. 205 at 19-20).

STANDARD FOR ADMISSIBILITY

Evaluation of expert testimony is guided by a trilogy of Supreme Court cases: *Daubert v. Merrell Dow Pharmaceuticals, Inc.,* 509 U.S. 579, 113 S.Ct. 2786, 125 L.Ed.2d 469 (1993); *Kumho Tire Co. v. Carmichael,* 526 U.S. 137, 141, 119 S.Ct. 1167, 143 L.Ed.2d 238 (1999); and *General Electric Co. v. Joiner,* 522 U.S. 136, 142, 118 S.Ct. 512, 139 L.Ed.2d 508 (1997). These cases clarify the district court's gatekeeper role under Federal Rule of Evidence 702. *United States v. Lauder,* 409 F.3d 1254, 1262 (10th Cir. 2005). Under Rule 702, a district court must satisfy itself that the proposed expert testimony is both reliable and relevant, in that it will assist the trier of fact, before permitting a jury to assess such testimony. *See* Fed.R.Evid. 702 ("If scientific, technical, or other specialized *knowledge will assist the trier of fact* to understand the evidence or to determine a fact in issue, a *witness qualified as an expert* by knowledge, skill experience, training or education may testify" at trial.) (emphasis added). "The proponent of expert testimony bears the burden of showing that its proffered expert's testimony is admissible." *United States v. Nacchio*, 555 F.3d 1234, 1241 (10th Cir. 2009); *see also Conroy v. Vilsack*, 707 F.3d 1163, 1168 (10th Cir. 2013). However, "[a] review of the caselaw after *Daubert* shows that the rejection of expert testimony is the exception rather than the rule . . . the trial court's role as gatekeeper is not intended to serve as a replacement for the adversary system. *United States v. McCluskey*, 954 F. Supp. 2d 1224, 1238 (D.N.M. 2013) (quoting Fed.R.Evid. 702 advisory committee's note to 2000 amendment).

As to reliability, this Court "assess[es] the reasoning and methodology underlying the expert's opinion . . . " *Dodge v. Cotter Corp.,* 328 F.3d 1212, 1221 (10th Cir. 2003) (quoting *Daubert,* 509 U.S. at 592–93). "[A]n expert's scientific testimony must be based on scientific knowledge, which 'implies a grounding in the methods and procedures of science' based on actual knowledge, not 'subjective belief or unsupported speculation.'" *Id.* at 1222 (quoting *Daubert,* 509 U.S. at 590). In *Daubert* the Supreme Court identified four nonexclusive factors a trial court may consider in making its reliability assessment: (1) whether the theory at issue can be and has been tested; (2) whether the theory has been subjected to peer review and publication; (3) whether there is a known or potential rate of error and whether there are standards controlling the methodology's operation; and (4) whether the theory has been accepted in the relevant scientific community. *Daubert,* 509 U.S. at 593–94; *Dodge,* 328 F.3d at 1222.

Assuming the reliability prong is met, the court must then assess other non-exclusive factors to determine whether the testimony will assist the trier of fact: (1) whether the testimony is relevant; (2) whether it is within the juror's common knowledge and experience; and (3) whether it will usurp the juror's role of evaluating a witness's credibility. In essence, the question is "whether [the] reasoning or methodology properly can be applied to the facts in issue." *Daubert,* 509 U.S. at 593; *see also United States v. Rodriguez-Felix*, 450 F.3d 1117, 1122–23 (10th Cir. 2006).

DISCUSSION

Defendant Oldman seeks to exclude expert testimony on STRmix™ generated DNA inclusion or match statistics for Items 12 and 53. Specifically, he contends that the FBI Lab's determination that the DNA mixture is composed of four individuals' DNA is not

reliable and that the FBI lab has not validated testing of mixtures with composition ratios as extreme as those in this case.[1] Before addressing Defendant's specific challenges, the Court outlines the information necessary to appreciate his arguments.

I. Probabilistic Genotyping Software

Some oversimplification of the science involving DNA is instructive:

> Within a typical human cell, DNA is wrapped tightly into forty-six chromosomes – often discussed as pairs of twenty-three. Physical locations ["loci" plural or "locus" singular] on one chromosome correspond with physical locations on the other paired chromosome. One [locus] location may specify that a person have brown eyes, the other corresponding location may specify blue. Or, both locations may specify blue, or both brown. How those genetic locations interact with each other ultimately determines your eye color. The important takeaway is that for each location on a chromosome that influences an attribute, there is a related location on its paired chromosome that also influences the attribute. The DNA found at one of those locations [locus] is called an "allele," and alleles, like chromosomes, come in pairs. [If a person has alleles that match at a given locus, they are homozygous if the alleles are different, they are heterozygous].
>
> Scientists have determined that certain alleles are highly variable between individuals. They have also determined the statistical probability of finding those alleles in the greater population. Thus, when a profile of alleles from a known person matches a profile of alleles from an unknown DNA sample, statistical analysis can give us insight into how likely it is that the known person is the source of the unknown DNA.
>
> A simplified example makes the point. Scientists know Joe Smith has a certain DNA profile. At locus 1, he has alleles A and B. At locus 2, he has alleles C and D. At locus 3, he has an unknown allele and E. Scientists also know that in the general population of men, 5% have the combination of A and B alleles at locus 1; 10% of men have the combination of C and D at locus 2, and 50% of men have the combination of a random allele and E at locus 3.
>
> Simple math explains how likely it is to find a person just like Joe in the general population of men. You multiply the percentages together: .05 × .10 × .50 = .00025 or .025% of the general population has the same genetic makeup as Joe Smith at those three loci.

[1] Defendant Oldman does not challenge the FBI analyst, Ms. Garfinkle, or her use of STRmix™ generally or the reliability of STRmix™ as a whole "when utilized within the parameters of a lab's internal validation." (ECF No. 207 at 2.)

> The math gets more complicated in the real world, but the concept remains the same. If you know the frequency of certain alleles appearing at certain locations, and those alleles match a known suspect, you can calculate how likely it is that the allele came from the suspect or from someone in the general population.

United States v. Barton, 2016 WL 11469438, at *1–2 (M.D. Fla. Sept. 10, 2016) (bracketed material added). The math and concepts become more complex when you have a mixture of DNA from more than one person. This complexity is where probabilistic genotyping software comes in and gives rise to the issues in this case.

Defendant Oldman challenges the use of a probabilistic genotyping software, STRMix™, as applied to his case. A 2016 report by the President's Council of Advisors on Science and Technology frames the issue nicely:

> DNA analysis of complex mixtures—defined as mixtures with more than two contributors—is inherently difficult and even more for small amounts of DNA. Such samples result in a DNA profile that superimposes multiple individual DNA profiles. Interpreting a mixed profiles is different for multiple reasons: each individual may contribute two, one or zero alleles at each locus; the alleles may overlap with one another; the peak heights may differ considerably, owing to differences in the amount and state of preservation of the DNA from each source; and the "stutter peaks" that surround alleles (common artifacts of the DNA amplification process) can obscure alleles that are present or suggest alleles that are not present. It is often impossible to tell with certainty which alleles are present in the mixture of how many separate individuals contributed to the mixture, let alone accurately to infer the DNA profile of each individual.
>
> Instead examiners must ask: "Could a suspect's DNA profile be present *within* the mixture profile? And, what is the probability that such an observation might occur by chance?"

President's Council of Advisors on Science and Technology (PCAST) (2016), *Forensic Science in the Criminal Courts: Ensuring Scientific Validity of Feature-Comparison Methods*, 1, 75–76, Executive Office of the President, Washington, D.C. ("PCAST Report"). After struggles with subjective interpretation of these types of samples, "several

groups have launched efforts to develop 'probabilistic genotyping' computer programs that apply various algorithms to interpret complex mixtures." *Id.* at 78. The two most widely used of those programs are STRmix™ and TrueAllele." § 30:33. *Special topics—Probabilistic software*, 4 Mod. Sci. Evidence § 30:33 (2018-2019 Edition).

"The FBI Laboratory began using the STRmix™ program . . . in December 2015." PCAST Report at 79; *see also* Daubert Hr'g Tr., December 21, 2018, (Testimony of Jerrilyn Conway).[2] The software "aims to use sophisticated modeling techniques to calculate digitally a statistic too complex to execute by hand." § 30:33. *Special topics—Probabilistic software*. "Each program has its own approach to calculating match statistics, and how it treats variables such as peak height, stutter, allele overlap, the probability of drop-out or drop-in, the impact of relatives, the number of contributors, and the like." *Id.*; *see also* § 11:7. *Admissibility of DNA typing technology*, Forensic DNA Evidence: Science and the Law § 11:7. While the PCAST Report recognizes these software programs as a major improvement in analyzing complex mixtures, it cautions "they still require careful scrutiny to determine (1) whether the methods are scientifically valid, including defining the limitations on their reliability (that is, the circumstances in which they may yield unreliable results) and (2) whether the software correctly implements the methods. This is particularly important because the programs employ different mathematical algorithms and can yield different results for the same mixture profile." PCAST Report at 79. As of the September 2016 PCAT Report,

> current studies have adequately explored only a limited range of mixture types (with respect to number of contributors, ratio of minor contributors,

[2] The transcript of the Daubert hearing held on December 21, 2018, has not yet been filed but will be available and filed at a later date. (*See* ECF No. 211.)

> and total amount of DNA). The two most widely used methods (STRmix™ and TrueAllele) appear to be reliable within a certain range, based on the available evidence and the inherent difficulty of the problem. Specifically, these methods appear to be reliable for three-person mixtures in which the minor contributor constitutes at least 20 percent of the intact DNA of the mixture and in which the DNA exceeds the minimum level required for the method.

Id. at 80. "[F]oundational validity must be established with respect to a specified method applied to a specified range." *Id.* at 81. However, more recent studies cast some doubt on the current accuracy of this proclamation.

> Recently, the internal validation data from 31 laboratories using or validating STRmix™ were compiled and interpreted specifically to address the points raised within the PCAST Report. This study concluded that this combined dataset "demonstrates a foundational validity of, at least, the STRmix™ software method for complex, mixed DNA probabilities to level well beyond the complexity and contribution levels suggested by PCAST." These efforts, representing a substantial resource commitment, are a collation of the validation studies from 31 laboratories and demonstrate that there is support for interpreting a minor contributor much less than 20%, and in fact down to 0% (present but not observed), of the total DNA present in the mixture.

John S. Buckleton, et al., *The Probabilistic Genotyping Software STRmix: Utility and Evidence for its Validity*, J. Forensic Sci. 1, 5 (2018).

II. Reliability of Number of Contributors Input Determination

First, Defendant Oldman challenges the reliability, and thus foundational validity, of the determination of the number of contributors to the samples in this case. Foundational validity requires "that it be shown, based on empirical studies" that a method is "repeatable, reproducible, and accurate, at levels that have been measured and are appropriate to the intended application."[3] *Id.* at 4. This scientific concept corresponds to Federal Rule of

[3] Reliability is defined as repeatability, reproducibility, and accuracy. PCAST at 47. Repeatable means "with known probability, an examiner obtains the same result, when analyzing samples from the same sources." *Id.* Reproducible is defined as "with known probability, different examiners obtain the same

Evidence 702(c) requiring "reliable principles and methods." *Id.* at 5. Again, in assessing reliability the Court considers: (1) whether the theory at issue can be and has been tested; (2) whether the theory has been subjected to peer review and publication; (3) whether there is a known or potential rate of error and whether there are standards controlling the methodology's operation; and (4) whether the theory has been accepted in the relevant scientific community. *Daubert,* 509 U.S. at 593–94.

As summarized by Ms. Conway during the Daubert hearing, with the exception of identical twins, the DNA of each individual is unique. This uniqueness allows scientists to look at different physical locations (locus) on a cell's DNA. Each locus has a specific DNA code, referred to as an "allele". In performing DNA testing the alleles at 21 different loci, known to vary among individuals, is used to create a DNA profile. *See United States v. Barton*, --- F.3d ---, 2018 WL 6374201 at 2-3 (11th Cir. December 6, 2018). A DNA profile is obtained by the use of an electropherogram, which charts or graphs as peaks the alleles at each of the 21 different loci. *Id.* at 3. The results of this process for Items 12 and 53 are attached as Exhibits E and F respectively to Defendant's Motion to Exclude (ECF No. 184-5 and 184-6); *see also* Daubert Hr'g Exhibits H and I.

There are two "basic" types of DNA profiles, single source (involving the DNA of only one person) and mixture or complex DNA (involving the DNA mixture of two or more individuals). Items 12 and 53 involved DNA mixtures and, as determined by the FBI

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result, when analyzing the same samples." *Id.* Accurate means "with known probabilities, an examiner obtains correct results both (1) for samples from the same source (true positives) and (2) for samples from different sources (true negatives). *Id.*

analyst, the DNA profiles obtained from these items was apparently comprised of four people. (ECF No. 184-2 at 6 and 9).

As summarized by Ms. Conway, who was the technical reviewer of the FBI laboratory report in this case (ECF No. 184-2), upon receipt of the DNA profile:

> the analyst first goes through a process of just count -- it's a simple procedure of counting the results at each location. So if you can imagine if there's a two-person mixture, this there should be no more than four results at each location. If there's a three-person mixture there should be no more than six results at each location. A simple count of the number of results at each location gives you a starting place to determine if that's -- if that then is the right number of contributors but then additional information is taken into account. When we look at the graph that has the results on it, those -- they're called peaks on the graph and we look at the balance of those peaks. We look at whether the ratios of contributors that we think is appropriate for the mixture is satisfied and if not, then there may be an additional person that's present. And so we'll look at that profile and say okay, we started at three now we're at four. So then we look at the profile to determine whether a fifth person should be added. And in this case, there's no apparent fifth person in this mixture. There's certainly a mix of four individuals but there's no obvious fifth person in this mixture. So the conclusion for this mixture was that there are four individuals present.

Ms. Conway further testified how a determination as to four apparent DNA contributors was made in this case:

> Q. When you look at multiple locations -- you said you look at 21 locations; is that correct?
> A. That's correct.
> Q. And in looking at those 21 locations, that is how you determine if it's a mixture; correct?
> A. Going through each of those locations in a very systematic way, yes, we determined that it's a mixture.
> Q. And in this case why do you believe there are four – four contributors, four DNA contributors?
> A. It's based on the number of results at each location as well as the balance or the heights of those different results. And using that information and looking at the mixture, it's apparent that there are -- that there are four individuals.

Ms. Conway also verified that the FBI Lab's internal validation, with the use of the GlobalFiler[4] amplification kit, covers up to apparent four-person mixtures:

> Q. And is the FBI crime lab accredited and validated to do four-person -- to determine if there's four people mixtures?
> A. We are validation covered for four-person mixtures. So when we looked at our -- when we did our internal validation of this kit, which is the test that we run, the 21 different locations, when we looked at our internal validation did cover four individuals, yes.

Id. Ms. Conway testified that the analyst calculates and then inputs the apparent number of contributors (2-4) into the STRmix™ program. STRmix™ then determines information about each of the individual contributors and optimizes the amount that each contributor may have donated to the sample. In addition to being validated to run these tests the FBI Lab, including the DNA unit, is accredited by the ANAB, ANSI-ASQ National Accreditation Board. (Conway Daubert Hr'g Testimony.). After going online with GlobalFiler® and STRmix™ version 2.4 the FBI Lab's validation study was reviewed by external auditors from the Florida Department of law enforcement. *Id.* Finally, Ms. Conway testified that specific to the validation of probabilistic genotypes systems, the FBI Lab's validations of GlobalFiler® and STRmix™ version 2.4 are in compliance with the Scientific Working Group on DNA Analysis Methods (SWGDAM) guidelines. *Id.* Based upon a review of the parties' submissions, applicable case law and Ms. Conway's testimony there is no basis to conclude the use of the GlobalFiler® Amplification Kit and

[4] The FBI Lab originally came on line with STRmix™ version 2.3 which analyzed DNA profiles from an Identifiler™ Amplification Kit that only amplified 15 different loci. In this case the FBI Lab used The GlobalFiler® PCR Amplification Kit that amplifies 21 different loci, the results of which are then run through STRmix™ version 2.4. (Conway Daubert Tr., December 21, 2018). Both GlobalFiler® Kit and STRmix™ version 2.4 have been validated and the tests run on Items 12 and 53. *Id*; *see also* Daubert Hr'g Exhibit E, Study Plan Summary—Validation of STRmix™ v2.4 for use with GlobalFiler™ DNA Typing Results Generated on the 3500xL.

STRmix™ version 2.4 on an apparent four person DNA mixture was outside the FBI Lab's validation and unreliable.

The real issue is not the process or software, both of which this court finds are scientifically valid, proven and tested. Rather, the real issue is whether the FBI analyst correctly interpreted the data, which includes the number of alleles at each locus compared to others and peak height, to concluded that the mixed DNA profiles from Items 12 and 53 were apparent four people, as opposed to five or three. (See Conway Daubert Hr'g Tr.). Ms. Conway testified that while STRmix™ itself doesn't account for any error in the apparent number of contributors, there are diagnostics reported by STRmix™ after a run is completed that an analyst can review, including the weights given to potential combinations of genotypes, to determine if there may be an error in the apparent number used. *Id.* In this case the results of the STRmix™ runs on Items 12 and 53 did not indicate any errors, intuitive or otherwise, that suggest the mixture was other than an apparent four person. *Id.*

Ms. Conway testified that not all DNA mixtures are the same and some are more difficult to determine the apparent number of contributors:

> Q. And so would it be accurate to say that some apparent four-person mixtures are easier to determine than others? Are all apparent four-person mixtures created equal?
> A. They're not, no.
> Q. And so in this case are you confident with regard to lab item number 12 that it was an apparent four-person mixture?
> A. Yes, I am.
> Q. And could you just explain to the Court briefly why you think that's the case.
> A. So looking at this mixture as a whole, the number of results at any given location was not more than six, which suggests that there are certainly three individuals in this mixture. Going further and looking at the balance of those results and the information throughout the mixture, there was

> apparently an additional contributor. There's no evidence in either of these profiles of a fifth contributor, which means that either there is no fifth contributor or that fifth contributor is at such a low level as to not impact the way that the rest of the profile is considered. So for both of these samples, there are apparently four individuals and we ran STRmix™ under that assumption.

Id. While Defense counsel effectively demonstrated that various studies have shown errors can be and have been made in determining the apparent number of contributors, nothing specific to Items 12 and 53 suggest the apparent number of contributors was erroneously calculated. Defendant's expert, Dr. Krane, testified that the genotyping results for Items 12 and 53 was consistent with the presence of at least four contributors. (See Daubert Hr'g Tr. Krane). Dr. Krane further testified that he accepted Ms. Conway's position that by looking at the electropherogram it appears to be a four-person mixture and "[t]here's no affirmative indication that it is a five-person mixture or six-person mixture or more." *Id.* Nonetheless, Dr. Krane noted nothing can be known with absolute one hundred percent certainty and it could be other than a four-person mixture. However, absolute certainty is not required for admissibility. Hence, while certainly fertile grounds for cross examination, such potential flaws in generally reliable scientific evidence is the purpose for which cross-examination exists. *See United States v. Barton*, *supra* at 6. In addition, the potential for error is reduced by the use of the GlobalFiler® PCR Amplification Kit, which collects data from 21 different loci, as opposed to 15 used in previous testing and studies.

Finally, in this case any error in the apparent number of contributors would only appear to modify the likelihood ratio to Defendant's benefit. Ms. Conway testified that if the DNA profile was really a three person mixture as opposed to a four, the likelihood

ratios would increase. *Id.* However, Ms. Conway noted that if the apparent number of contributors was five as opposed to four the literature is clear that the result would either be the same likelihood ratio or more conservative. *Id.* Ms. Conway's testimony is consistent with the scientific literature:

> With this general process, a reasonable NoC [number of contributors] can be assigned, but there is no guarantee that this estimate is the actual NoC of the sample. Confidence in the assignment varies depending on the complexity of the mixture. Fortunately, any reasonable discrepancy in NoC assignment seems to have a minor effect on the deconvolution or LR [likelihood ratio].

John S. Buckleton, et al., *The Probabilistic Genotyping Software STRmix: Utility and Evidence for its Validity*, J. Forensic Sci. 1, 9 (2018)(See Exhibit No. 5 to Gov't Response; ECF No. 205-4 at 9). Dr. Buckleton concluded:

> "Overestimation of N generally led to similar or lower LRs for true contributors. Underestimation of N resulted in exclusions of true contributors, usually affecting the lower/lowest quality contributor(s). This data supports the view that when assigning N, for false contributors, the risk is overestimation of N, as there is an increase in the number of very low-grade adventitious hits. With respect to the LR for true contributors, when N is either under or overestimated, the result is conservative."

Id. This conclusion is consistent with the most recent reported study. *See* Bright J-A, Richards R, Kruijver M, Kelly H, McGovern C, Magee A, et al., *Internal Validation of STRmix™ -- A multi-laboratory Response to PCAST*; Forensic Science International: Genetics 34 (2018) at 11-14 (attached as Exhibit 10 to Gov't Response; ECF No. 205-10 at 11-14).

Based upon the foregoing this Court finds that the STRmix™ results for Items 12 and 53 have been derived from a scientifically valid, reliable and tested methodology and are admissible. Defendant's argument as to any error in the apparent number of

contributors used in analyzing the DNA mixtures for Items 12 and 53 goes to the weight, not their admissibility. *See Barton, supra.* at 5-6.

III. Validation of Extreme Ratios

Defendant Oldman also contends that the FBI lab has only validated STRmix™ up to a 10:1 ratio of the largest to smallest DNA contributor amounts. Thus, Defendant asserts any ratio in excess of 10:1 is not reliable. In this case, the swab from the basement stairs had a ratio of 18:1 and the sample on Oldman's shirt had a ratio of 15:1 (ECF No. 184 at 36). The Court finds that any discrepancy in the ratios does not render Items 12 and 53 inadmissible.

Ms. Conway testified that both Items 12 and 53 were done in accordance with and within the FBI Lab's validation for STRmix™ version 2.4. (Daubert Hr'g Testimony). Moreover, Ms. Conway testified that the proportion of contributors to the mixture is different and is not equally comparable. *Id.* at 42. Dr. Kane testified that at higher ratios there is greater risk of stutter peaks from a major contributor being confused with peaks from minor contributors. (Daubert Hr'g at 103.) Dr. Kane testified that the largest validation ratio done in the FBI's validation of STRmix™ 2.4 version (Daubert Hr'g Exhibit E) was a 10:1 ratio. *Id.* at 103. Dr. Krane felt that the ratio between the major and minor contributor in Items 12 and 53 was significantly outside the range of the FBI Lab's validation summary and, therefore, he didn't feel comfortable in saying this validation summary supports the use of STRmix™ version 2.4 in this case. Nonetheless, Dr. Krane did not identify any irregularities with the electropherogram or other concerns with miscalculation or confusion of stutter peaks.

Ultimately, based upon the testimony and scientific studies, it does not appear to this Court that the ratio variance between the FBI Lab's validation study and Items 12 and 53 render the results unreliable or inadmissible. While admittedly an oversimplification, it appears to this Court the effect is that the higher the ratio between the major and minor contributor, the higher potential for error in calculating the ratio occurs, particularly in low quality DNA, due to the stutter effect. However, that does not appear to invalidate the identity of the DNA makeup or likelihood ratios. In the end this Court finds the issue goes to the weight, not the admissibility of the evidence. *See Stills v. Dorsey*, 7 Fed.Appx. 856, 2001 WL 303351 at 2 (10th Cir. March 29, 2001) (defendant's objection to reliability of DNA analysis goes to weight rather than admissibility); *see also United States v. Barton*, *supra* at 6-7. Items 12 and 53 are admissible. Any discrepancy with the FBI Lab's validation study are matters for cross examination.

Conclusion

Considering those standards set forth under *Daubert*, this Court finds the STRmix™ test results for Items 12 and 53 are based upon a tested and valid scientific methodology that is generally accepted by the scientific community[5] and has been subject to peer review and standards sufficient to ensure its reliability and admissibility. The United States has

[5] In 2018 State and Federal Courts generally addressing the admissibility of probabilistic genotyping software, specifically STRmix™ have found it admissible. *See United States v. Lee*, ---Fed.Appx. --- 2018 WL 6600956 (2nd Cir. Dec. 14, 2018); *People v. Superior Court (Dominguez)*, 28 Cal.App.5th 223, 2018 WL 5023571(Oct. 2018); *People v. Smith*, 2018 WL 4926977 (Mich. Court of App., Oct. 9, 2018); *People v. Muhammad*, ---N.W.2d ---, 2018 WL 4927094 (Mich. Court of App., Oct. 2, 2018); *People v. Blash*, 2018 WL 4062322 (Superior Court of Virg. Islands, Aug. 24, 2018); *People v. Seepersad*, 58 Msc.3d 1227(A), 2018 WL 1163820 (NY Supreme Court, March 5, 2018); *People v. Juan Manuel Venegas*, 17-CR-2383 (Calif. Superior Court, Shasta County, Nov. 6, 2018). A summary of labs utilizing STRmix™, peer reviewed publications and cases addressing the admissibility of STRmix™ results can be found at https://johnbuckleton.wordpress.com/strmix/ (last visited December 31, 2018).

established, by a preponderance of the evidence, the admissibility of these Items. Therefore:

It is hereby ORDERED that Defendant's Motion to Exclude Expert Testimony on STRmix™ Generated DNA Inclusion or Match Statistic Under Daubert and Federal Rules of Evidence 703 (ECF No. 184) is hereby DENIED.

Dated this 31ST day of December, 2018.

Scott W. Skavdahl
United States District Judge